

```

5' AAA CCT TCA CCT CTC ATG CTG AAG CTC ACA CCC TTG CCC TCC AAG ATG AAG GTT 54
    M L K L T P L P S K K M K V
      9      18      27      36      45
      63      72      81      90      99      108
TCT GCA GCG CTT CTG TGC CTG CTG CTC ATG GCA GCC ACT TTC AGC CCT CAG GGA
S A A L L C L L L L M A A T F S S P Q G
      117      126      135      144      153      162
CTT GCT CAG CCA GAT TCA GTT TCC ATT CCA ATC ACC TGC TGC TTT AAC GTG ATC
L A Q P D S V S I P I T C C F N V I
      171      180      189      198      207      216
AAT AGG AAA ATT CCT ATC CAG AGG CTG GAG AGC TAC ACA AGA ATC ACC AAC ATC
N R K I P I Q R L E S Y T R I T N I
      225      234      243      252      261      270
CAA TGT CCC AAG GAA GCT GTG ATC TTC AAG ACC AAA CGG GGC AAG GAG GTC TGT
Q C P K E A V I F K T K R G K E V C
      279      288      297      306      315      324
GCT GAC CCC AAG GAG AGA TGG GTC AGG GAT TCC ATG AAG CAT CTG GAC CAA ATA
A D P K E R W V R D S M K H L D Q I
      333      342      351      360      369      378
TTT CAA AAT CTG AAG CCA TGA GCC TTC ATA CAT GGA CTG AGA GTC AGA GCT TGA
F Q N L K P

```

FIGURE 1A

387 396 405 414 423 432
AGA AAA GCT TAT TTA TTT TCC CCA ACC TCC CCC AGG TGC AGT GTG ACA TTA TTT

441 450 459 468 477 486
TAT TAT AAC ATC CAC AAA GAG ATT ATT TTT AAA TAA TTT AAA GCA TAA TAT TTC

495 504 513 522 531 540
TTA AAA AGT ATT TAA TTA TAT TAT TGT TGA TGT TTT AAC TCT ATC TGT CAT

549 558 567 576 585 594
ACA TCC TAG TGA ATG TAA AAT GCA AAA TCC TGG TGA TGT GTT TTT TGT TGT

603 612 621 630 639 648
TTT CCT GTG AGC TCA ACT AAG TTC ACG GCC AAA NGT CAT TGT TCT CCC TCC TAC

657 666 675 684 693 702
CNG TNC GTA GTG TTG TGG GGT CCT CCC NTG GAT CAT CAA GGT GAA ACA CTT AGG

711 720 729 738 747 756
TAT TCT TTG GCA ATC AGT GCT CCT GTA AGT CAA ATG TGT GCT TTG TAC TGC TGT

765 774 783 792 801 810
TGT TGA AAT TGA NGT TAC TGT ANA TAA CTA TGG AAT TTT GAA AAA AAA TTT CAA

819 828 837 846 855
AAA GAA AAA NAT ATA TAT AAT TTA AAA CTA AAA AAA AAA AAA A 3'

FIGURE 1B

1	M	L	K	L	T	P	L	P	S	K	M	K	V	S	A	A	L	L	C	L	L	L	L	M	A	A	T	F	S	P	Q	G	L	A	Q	P	D	S	V	S	I	965517
1	M	W	K	P	M	P	S	P	S	N	M	K	A	S	A	A	L	L	C	L	L	L	L	T	A	A	A	F	S	P	Q	G	L	A	Q	P	V	G	I	N	T	GI 288397
1	M	-	-	-	-	-	-	-	-	-	-	K	V	S	A	A	L	L	C	L	L	L	I	A	A	T	F	I	P	Q	G	L	A	Q	P	D	A	I	N	A	GI 338809	
41	P	I	T	C	C	F	N	V	I	N	R	K	I	P	I	Q	R	L	E	S	Y	T	R	I	T	N	I	Q	C	P	K	E	A	V	I	F	K	T	K	R	965517	
41	S	T	T	C	C	Y	R	F	I	N	K	I	P	K	I	Q	R	L	E	S	Y	R	R	T	T	S	S	H	C	P	R	E	A	V	I	F	K	T	K	L	GI 288397	
31	P	V	T	C	C	Y	N	E	T	N	R	K	I	S	V	Q	R	L	A	S	Y	R	R	I	T	S	S	K	C	P	K	E	A	V	I	F	K	T	I	V	GI 338809	
81	G	K	E	V	C	A	D	P	K	E	R	W	V	R	D	S	M	K	H	L	D	Q	I	F	Q	N	L	K	P											965517		
81	D	K	E	I	C	A	D	P	T	Q	K	W	V	Q	D	F	M	K	H	L	D	K	K	T	Q	T	P	K	L											GI 288397		
71	A	K	E	I	C	A	D	P	K	Q	K	W	V	Q	D	S	M	D	H	L	D	K	Q	T	Q	T	P	K	T											GI 338809		

FIGURE 2

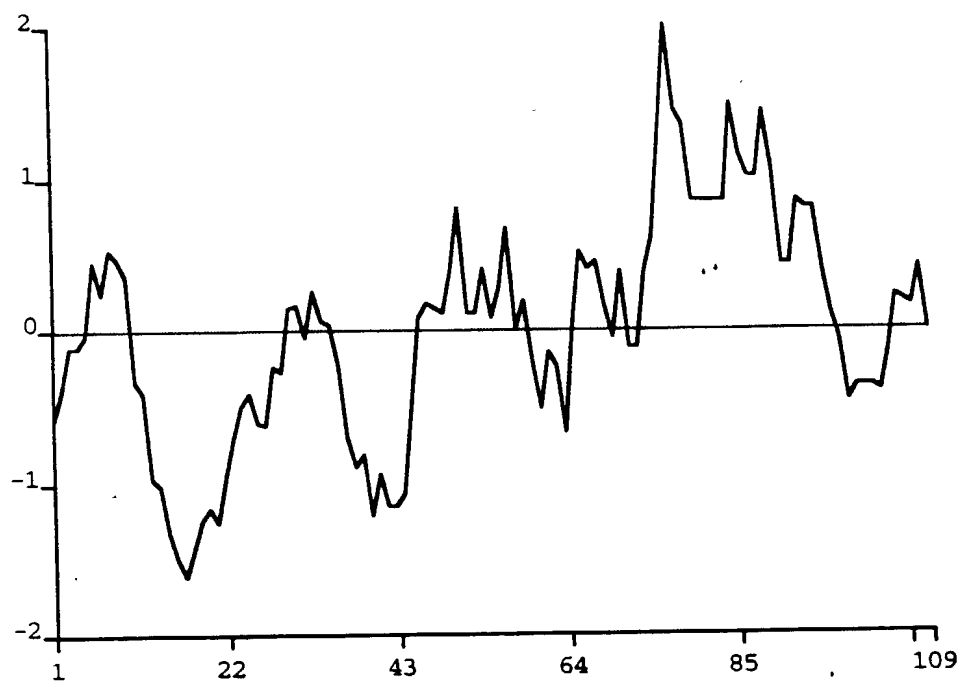


FIGURE 3

Title: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROPROTEIN

Serial No.: 10/033,067

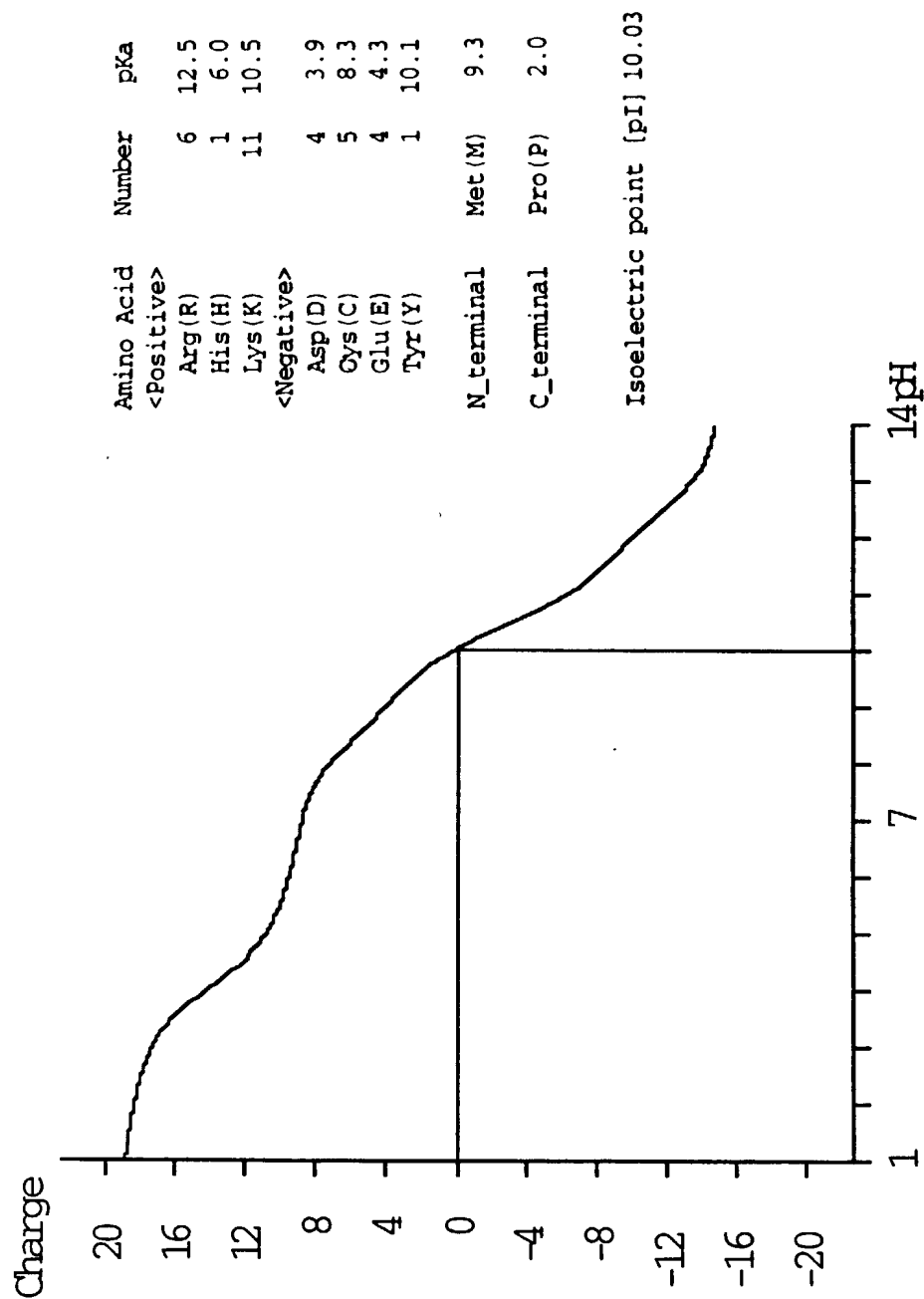


FIGURE 4

The Electronic Northern for clone: 965517
and Stringency = 50

Library	Lib Description	Abun	Pct Abun
<u>PANCDIT03</u>	pancrease, NIDDM, 57 M	1	0.145
<u>MMLR1DT01</u>	macrophages (adher PBMNC), M/F, 24-hr MLR	4	0.094
<u>MMLR3DT01</u>	macrophages (adher PBMNC), M/F, 72-hr MLR	2	0.066
<u>MPGHLPT02</u>	macrophages (adher PBMNC), M/F, treated LPS	1	0.049
<u>TMLR3DT01</u>	lymphocytes (non-adher PBMNC), M, 96-hr MLR	2	0.045
<u>BLADTUT02</u>	bladder tumor, carcinoma, 80 F	1	0.030
<u>SYNORAT05</u>	synovium, knee, rheumatiod, 62 F	1	0.028
<u>LUNGNOM01</u>	lung, 72 M, WM	1	0.026
<u>MPGHNOT03</u>	macrophages (adher PBMNC), M/F	2	0.025
<u>BRSTNOT05</u>	breast, 58 F, match to BRSTTUT03	1	0.015

FIGURE 5